SEQUENCE LISTING

<110> Madden, Mark
Weiner, David P.
Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> Not yet known
<141> 2000-12-28

<150> 60/254,414
<151> 2000-12-07

<150> 60/173,609
<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1
<211> 1041
<212> DNA
<213> Unknown Organism

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<223> Description of Unknown Organism: Obtained from an environmental sample

<220>
<221> CDS
<222> (1)..(1041)

<400> 1

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atg tcg gag ccc atg acg aag tat cgc ggc gcg gcg gtg cag gcc gcg   48
Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala
  1               5                  10                  15

ccg gtg ttc ctc gat ctc gac cgc aca gtc gag aaa gcg atc ggc ctg   96
Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu
            20                  25                  30

atc gag cag gcg gcc aag cag gac gtg cgc ctg atc gca ttc cca gag   144
Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu
        35                  40                  45

act tgg att ccc ggc tat ccc ttt tgg ata tgg ctg ggc gcg ccg gct   192
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala
    50                  55                  60

tgg ggc atg cgc ttc gtc cag cgc tat ttc gag aat tcg ctc gtg cgc   240
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg
65                  70                  75                  80

ggc agc aag cag tgg cag gcc ctg gcg gat gcg gcc cgc cgc cac ggc   288
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly
                85                  90                  95

atg cat gtc gtg gcc ggc tat agc gag cgc gcg ggc ggc agc ctc tat   336
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr
            100                 105                 110
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atg ggc cag gcg atc ttc ggc ccc gat ggc gat ctg atc gcc gcg cgc   384
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg
        115                 120                 125

cgc aag ctc aag cct acc cat gcg gag cgc acc gtg ttc ggc gag gga   432
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly
    130                 135                 140

gac ggc agc cat ctc gcg gtg cac gat acc gcc atc ggg cgc ctc ggc   480
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly
145                 150                 155                 160

gcg ctc tgt tgc tgg gag cac atc cag cca ttg tcg aaa tac gcc atg   528
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met
                165                 170                 175

tac gcc gcc gac gaa cag gtc cac gtc gcg tcg tgg ccg agc ttc agc   576
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser
            180                 185                 190

ctc tat cgc ggc atg gcc tat gcg ctc gga ccg gag gtc aat acc gcc   624
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala
        195                 200                 205

gca agc cag atc tac gcg gtc gag ggc ggc tgc tac gtg ctg gcg tcg   672
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser
    210                 215                 220

tgc gcg acc gtt tcg ccg gag atg atc aag gta ttg gtg gat acg ccc   720
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro
225                 230                 235                 240

gac aag gag atg ttc ctc aag gcc ggc ggc ggt ttt gcc atg att ttc   768
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe
                245                 250                 255

ggg ccc gac ggc cgc gcc ctg gcc gag ccg ctc ccg gag acc gaa gag   816
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu
            260                 265                 270

gga ctg ctg gtc gcc gat atc gac ctc ggc atg atc gcg ttg gcc aag   864
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys
        275                 280                 285

gcg gcg gcc gat ccg gcg ggc cac tat tca cgg ccc gac gta acg cgg   912
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg
    290                 295                 300

ctg ctg ctg gat cga cgt ccg gcc caa cgc gtc gtc acg ctt gat gcc   960
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala
305                 310                 315                 320

gca ttc gaa ccg caa aac gag gac aag ggc gac gcg ccc gcg ctg cgc  1008
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg
                325                 330                 335

gtg gtg gcg gaa agc gcc gcc gcc gcg cag tag                      1041
Val Val Ala Glu Ser Ala Ala Ala Ala Gln
            340                 345
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<212> PRT

<213> Unknown Organism
<223> Description of Unknown Organism: Obtained from an
environmental sample

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Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu
20 25 30
Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu
35 40 45
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala
50 55 60
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg
65 70 75 80
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly
85 90 95
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr
100 105 110
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg
115 120 125
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly
130 135 140
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly
145 150 155 160
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met
165 170 175
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser
180 185 190
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala
195 200 205
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser
210 215 220
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro
225 230 235 240
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe
245 250 255
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu
260 265 270
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys
275 280 285
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg
290 295 300
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala
305 310 315 320
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg
325 330 335
Val Val Ala Glu Ser Ala Ala Ala Ala Gln
340 345

<210> 3
<211> 1014
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Obtained from an
environmental sample

<220>
<221> CDS
<222> (1)..(1014)

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<400> 3
atg aaa gaa gct atc aag gtc gcc tgc gtg caa gcc gcc ccg atc tac      48
Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr
  1               5                  10                  15

atg gat ttg gag gcg acg gtg gac aaa acc att gag ttg atg gaa gaa      96
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu
             20                  25                  30

gca gca cgt aat aat gct cgt ctg atc gcc ttt ccg gaa act tgg att     144
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
         35                  40                  45

cca ggc tac cca tgg ttt ctt tgg ctt gac tca cca gca tgg gca atg     192
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met
     50                  55                  60

caa ttt gta cgc caa tac cat gag aac tca ttg gag ttg gat ggc cct     240
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro
 65                  70                  75                  80

caa gct aag cgc att tca gat gca gcc aag cgg ttg gga atc atg gtc     288
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val
                 85                  90                  95

acc ctg ggg atg agt gaa cgg gtc ggt ggc acc ctt tac atc agt cag     336
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln
            100                 105                 110

tgg ttc ata ggc gat aat ggt gac acc att ggg gcc cgg cga aag ttg     384
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu
        115                 120                 125

aaa cct act ttt gtt gaa cgt act ttg ttc ggc gaa ggg gat ggt tca     432
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
    130                 135                 140

tcg cta gcg gtt ttc gag acg tct gtt gga agg ctg ggt ggc tta tgc     480
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys
145                 150                 155                 160

tgt tgg gag cac ctt caa ccg cta aca aaa tac gct ttg tat gca caa     528
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln
                165                 170                 175

aat gaa gag att cat tgt gcg gct tgg ccg agc ttt agc ctt tat cct     576
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro
            180                 185                 190

aat gcg gcg aaa gcc ctg ggg cct gat gtc aat gta gcg gcc tct cga     624
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg
        195                 200                 205

atc tat gcc gtt gaa ggg caa tgc ttc gta cta gcg tcg tgt gcg ctc     672
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
    210                 215                 220

gtt tca caa tcc atg atc gat atg ctt tgt aca gat gac gaa aag cat     720
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His
225                 230                 235                 240

gcg ttg ctt ctg gct ggt ggt gga cac tca cgt atc ata ggg cct gat     768
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp
                245                 250                 255
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ggt ggt gac ttg gtc gcg cct ctt gcc gaa aat gaa gag ggt att ctc 816
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu
260 265 270

tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca 864
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala
275 280 285

gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata 912
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile
290 295 300

gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt 960
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg
305 310 315 320

cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa 1008
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu
325 330 335

att tga 1014
Ile

<210> 4
<211> 337
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: Obtained from an environmental sample

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Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu
20 25 30
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
35 40 45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met
50 55 60
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro
65 70 75 80
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val
85 90 95
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln
100 105 110
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu
115 120 125
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
130 135 140
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys
145 150 155 160
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln
165 170 175
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro
180 185 190
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg
195 200 205
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
210 215 220
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His
225 230 235 240
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp
245 250 255
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu

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                260                           265                           270
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala
            275                     280                     285
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile
    290                     295                     300
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg
305                     310                     315                     320
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu
                    325                     330                     335
Ile
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